Uses of The RHIC Collimators

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Purpose of the Collimators

The purpose of the collimators is to remove the beam halo to protect the experiments and accelerator components (i.e. The Abort Kickers) from excess radiation. They are also used for "gap cleaning", i.e. remove the unbunched beam kicked by the tunemeter kicker from the abort gap. The purpose of the collimators is not to be a beam dump (using them as such may cause Permit problems, magnet quenches, and will eventually destroy the collimators).

It is hoped that the collimators will be transparent to operations except for gap cleaning. But there are a few times when they will not be, so below are lots of helpful hints on dealing with them. If there is a problem, Ray Fliller and Angelika Drees are the ones to call.
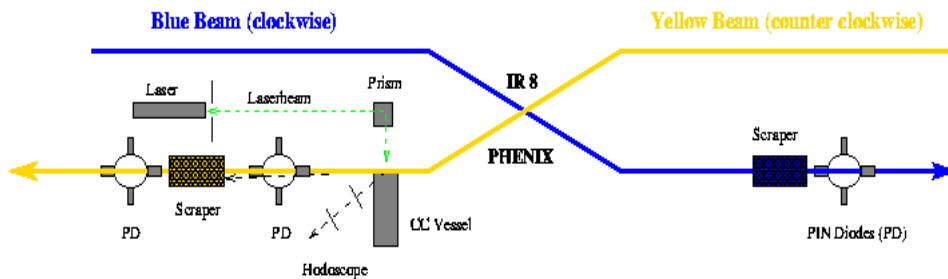

Figure 1: RHIC Collimation System

Description

- Location: The RHIC Collimators are located downstream of PHENIX in each ring, 7 o'clock side for Yellow, 8 o'clock side for Blue, each in the warm straight section between Q3 and Q4 at 591m and 686m.

- Material: The blue collimator consists of a 0.45m long, upside down L shaped Cu scraper. The Yellow collimators consist of similar Cu scraper and a 5mm long Si Crystal Collimator. The yellow crystal collimator is not operational at this point and should not be moved.. The scrapers allow transverse motion is the horizontal and vertical plane, and rotation about the vertical axis.

- Beam Loss Monitors: Downstream of both scrapers are 4 BLMS's that are used to measure the scattered particles from the scraper (the BLM's are not connected to BLAM or the Permit Link).

- PIN Diodes: Downstream of both scrapers is an array of 4 PIN diodes. Upstream of the yellow collimator are also 8 PIN diodes to measure particles scattered from the crystal. Theses are also 2 scintillators looking at the crystal of measure losses there.

- GPMs: There are two GPM's to be aware of under RHIC → Collimator, pindiodes.mon contains the loss rates seen at all of the PIN diodes in both rings. CollimatorPosition.mon gives readbacks of the Stepper Motor positions of the collimators (positions are also available in the pet pages). Collimation positions, and PIN diode rates are logged.

- PET Pages: There are two PET pages to control both scrapers and the crystal. They are under RHIC → Instrumentation → Collimator. For Blue use BlueScraper and for Yellow use YellowScraper. YellowScraper also contains the crystal controls.

- Sequencer: There are 5 sequences for the Collimators under RHIC → Collimator. Under the Yellow and Blue folders there are 2 sequences:

  - Home: Fully retracts that collimator.
  - LimAperture: Moves that scraper in to the nominal position for operations.

  There is also a separate Home sequence which will retract all collimators at once (crystal included).

Collimator Insertion

- The scrapers are always inserted automatically by RHIC → InstrumSetup → NewFill sequence (unless skipped over). The purpose of inserting them is to reduce losses at the abort kickers during the ramp and store. Since the kicker is a vertical aperture limit, the scrapers are vertically very far in, and horzontally in only enough to barely touch the beam.

- If there are still significant losses on the abort kicker, it is possible to insert the scrapers more by increasing the step command on the

horizontal or vertical axis (please increase by ≤ 1000 steps). Steps are counted in absolute number, not increment.

- The collimators are fully inserted in a particular plane when the "AtLimit?" on the PET page reads "outer" for X,Y,or Z. (horizontal,vertical,skew) This will most likely kill the beam but depends on the closed orbit (see orbit application)

Collimator Retraction

- The scrapers are retracted automatically on the RHIC $\rightarrow$ Ramp $\rightarrow$ DownToPark sequence. They are commanded out before the dump.

- If there is any reason to retract the collimators without fully pulling them out, just reduce the number in the step command in the horzontal or vertical plane (decrease by ≥ 1000 steps). Reducing the skew only changes the alignment, is not necessary for retraction, and could potentially move the edge of the jaw into the beam and cause higher losses.

- The collimators are fully retracted when the step rdbk is zero (or close to it) and the "AtLimit?" on the PET page reads "inner" for X,Y,and Z. All LVDT voltages (says mm, it is volts) should read $\approx 9.8V$. Please note: It is not necesary for the skew (Z) to be zero, horizontal and vertical are sufficient to remove the collimator from the beam.

Reasons to Retract Collimators

There are times when retracting the collimators a little for a short time may be a good idea.

- Large losses up the ramp, especially in the 8 o'clock are for blue losses, or 7 o'clock for yellow losses. Losses in other areas of the ring are most likely <u>not</u> caused by the collimators, but if in doubt, pull'em out. Always insert them again at the top. It is probably not a good idea to use the LimApperture sequence, as it will move the scrapers in quickly, and the sudden losses may pull the permit. So do it by hand (see below).

- Steering PHENIX. If extra losses are seen at the collimators during steering at PHENIX, retract them $\approx$ 10000 steps in the horizontal and vertical. Please reinsert them after steering PHENIX, just enough to reduce the losses at the abort kickers. This is not to discourage steering PHENIX, but to raise awareness of "mysterious" losses during steering.

- Lattice changes. If there is any change in the β^* at PHENIX or major tuning at store needs to be done, the collimators should be retracted fully (Home sequence), and skipped in the RHIC $\rightarrow$ InstrumSetup $\rightarrow$ NewFill sequence. Small corrections do not warrant retracting the collimators. If the β^* at PHENIX is changed, the collimators should not be inserted again until Ray or Angelika have had a chance to find new positions.

- Bad Lifetime. If beam mysteriously gets lost in the collimator area, they are blameful. But, if not **they are probably not the cause for bad lifetimes**. Of course, they are good candidates, but chromaticity, rebucketing, tune shifts, bad orbits, bad injection, RF trips, drifting power supplies,*etc.* have been reducing lifetimes long before the collimators where an issue. But if in doubt, pull'em out.

- Beam Studies. There are some studies which require that there is no scraping (IBS, Beam–Beam, *etc.*), the collimators can be retracted for this.

Gap Cleaning

There is a separate procedure for this. Please read it carefully.

Manually Moving the collimators

When using the collimators there are four displays that are crucial:

- pindiodes.mon: The PIN diodes are very sensitive to small losses that the BLM system will never see. For the blue collimator, use PIN Diodes Blue 1,3,4 (2 is virtually dead). These may have a large offset of $\approx$ 13500 this is O.K. and is not really beam loss, losses above this are real though. For Yellow look at PIN Diodes Yellow 1,2,3,4. These have no offset. The PIN diodes are useful when finding the beam with the collimators, and aligning the scraper skew.

- BLM Display: Once the BLM's can see steady losses at the collimators, it is necessary to watch the beam currents while using the collimators to make sure that you are not scraping away good beam.

- Beam Current Display: If you are affecting the lifetime, you are in too far.

- Pet page: The most important thing to note is the **PANIC** button. Any command given to the collimators will be completed before the next command is executed. So if you accidentally type in a step command that is too large – Hit the **PANIC** button **for that line**. The collimator will stop moving. Then you can give the proper command.

Whenever moving the collimators manually, pay close attention to above displays, you will be blamed for the death of a good store (even if the death has nothing to do with you – trust us, we know).

- Adjust the skew: It is important to adjust the horizontal skew of the scraper if it is not already done. The skew rotates the scraper in the horizontal plane, in an attempt to align the collimator to the beam envelope. It is important to get the skew close to optimal to increase the collimation efficiency. The sequence LimApperture puts the collimators to a close enough value (35000 steps). The gap cleaning procedure explains the finer points of skew alignment for the curious, but 35000 steps is close enough.
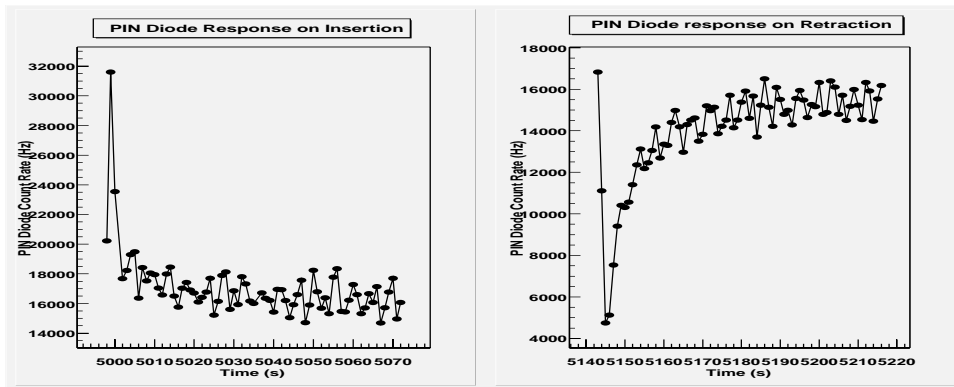

Figure 2: PIN Diode Response for insertion and retraction

- insert the scraper (never the crystal): (i.e. Increasing the step command on the horizontal or vertical),

    - At present, good start values are 12000 steps for horizontal, 60000 for vertical. Note: This can change with the orbit.

    - Watch the PIN diodes. Once the rates increase, the scraper is in the beam halo. Subsequent insertion of the scraper will show a large spike with a falloff as seen in figure 2. This is the inital scrape of the beam followed by beam diffusion. The steady state loss will be no less than before the insertion. There may even be a pulse in the BLM display if you are very far into the beam. On retraction of the scraper (i.e. Decreasing the step command on the horizontal or vertical), you will see a dropoff followed by a rise in the counts (assuming you are still in the beam) also seen in figure 2. The dropoff is you pulling out and the rise is the beam diffusion out to the collimator again. The steady state will be no greater than before you retracted.

    - Step the scraper to the step value you desire. When stepping in, do not increase by more that 2000 steps. When stepping out, move out as far as you wish.

    - Don't kill the beam. If the lifetime of the beam starts to decrease, retract the collimator a little. You are in too far. The goal is to reduce the losses at the abort kicker not to shorten the store.

    - Don't move the crystal collimator.